

0500/0240



OIEP

#2.

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/053,291

TIME: 09:32:54

Input Set : N:\Crf3\RULE60\10053291.raw

Output Set: N:\CRF3\02062002\J053291.raw

1 <110> APPLICANT: Stuhlmann, Heidi
 2 Xiong, Jing-Wei
 3 Taubman, Mark B.
 4 <120> TITLE OF INVENTION: VASCULAR ENDOTHELIAL ZINC FINGER 1 GENE
 5 AND PROTEIN AND USES THEREOF
 6 <130> FILE REFERENCE: 31200
 8 <140> CURRENT APPLICATION NUMBER: 10/053,291
 9 <141> CURRENT FILING DATE: 2002-01-17
 11 <150> PRIOR APPLICATION NUMBER: US/09/083,290A
 12 <151> PRIOR FILING DATE: 1998-05-22
 15 <160> NUMBER OF SEQ ID NOS: 13
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 3645
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Mus musculus
 22 <400> SEQUENCE: 1

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25	ctgcccctcc	tgagttctgc	tgtggagccc	cctgatcaga	aaccgttgct	tccaatacca	180
26	attactcaga	aacctcaggc	tgcaccagaa	acattaaagg	atgccattgg	gattaaaaaa	240
27	gaaaaaccca	aaacttcgtt	tgtgtgcact	tactgcagta	aagcattcag	ggacagctat	300
28	cacctgaggc	gccatcagtc	ctgccacaca	gggatcaagt	tgggtgtctcg	ggcaaagaaa	360
29	acccccacca	cggtgggtcc	ccttatctcc	accattgctg	gggacagcag	ccgaacttcg	420
30	ttggtttcaa	ctattgcagg	catcttgtea	acagtcacta	catcttcctc	gggcaccaac	480
31	cccagcagca	gcgctagtag	cacagcaatg	cctgtgcccc	agtctgtcaa	gaaacccagt	540
32	aagcctgtca	agaagaacca	cgectgtgag	atgtgtggga	aggccttccg	ggatgtgtac	600
33	cacctcaatc	ggcacaagct	ctcccattcg	gacgaaaagc	cctttgagtg	tcctatttgt	660
34	aatcagcgct	tcaagaggaa	ggaccggatg	acttaccatg	tgaggtctca	tgaaggaggc	720
35	atcaccaaac	cctatacttg	cagtgtttgt	gggaaaggct	tctcaaggcc	tgaccaccta	780
36	agctgtcatg	taaaacatgt	gcattcaaca	gaaagaccct	tcaaagcca	aacgtgcact	840
37	gctgccttgg	ccaccaaaga	cagactacgg	acacacatgg	tgcgccacga	aggcaaggta	900
38	tcatgtaaaca	tctgtgggaa	gctcttgagt	gcagcatata	tcaccagcca	cttaaagaca	960
39	catgggcaga	gccaaagtat	caactgtaac	acgtgcaaac	aaggcatcag	caaaacgtgc	1020
40	atgagttagg	agaccagcaa	tcagaagcag	cagcagcagc	agcagcaaca	gcagcagcag	1080
41	caacaacaac	aacatgtgac	aagctggcca	gggaagcagg	tagagacact	gagactgtgg	1140
42	gaagaagctg	tcaaagcaag	aaagaaagaa	gctgccaaac	tgtgccaaac	ctccacggct	1200
43	gctacgacac	cagtgactct	cactactcca	ttcaatataa	cgctctctgt	gtcgtctggg	1260
44	actatgtcaa	accagtcac	agtggcagct	gcaatgagca	tgagaagtcc	agtaaagtgc	1320
45	tcaagtgcag	ttaacataac	cagcccctta	gccatgacct	cacctttaac	actcaccacc	1380
46	ccagtcaacc	tccccacccc	tgtgaccgcc	ccagtgaata	tagcacaccc	tgccaccatc	1440
47	acatctccaa	tgaacctgcc	cactcctatg	acattagctg	cccctctcaa	tatagcaatg	1500
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50      gattaaagca aaaagcagac tatgaaattg ggaggtttta ttatgttagt taataagagt      1680
51      gtagtagctc caattttgct ggggttggtc aaagtagggg atagtgttaa cttatcactg      1740
52      gaccacttta gtttactcag aaaccctttt agctgacacc attgcttaaa caggatagta      1800
53      gctggcaaga cgaatgccca gaattaaaac caatcataaa acccatttca aaataaaaaa      1860
54      gcattatttg tttttattat ttttttaaat acaacagaat ctttttattg taaacactag      1920
55      cagagttcct ccctctgtac aagggtggacg gttttaacct ggagctcaag cccacagact      1980
56      gagagctagt gtagcattgt ctgtggtttt gctcgtatga gtgaacagag gcattgtcat      2040
57      aataaaatgc atttcagaga atatgcattt tacctttggg aatatgttaa ttccaggcag      2100
58      cattccctat gggaaagggt ataccagctc tgatatgcaa agcatatgat aatttatcat      2160
59      tctaacttca acatataata gggattgtga cctgatattt ggagatgtaa atattgctca      2220
60      gcatattaat ccctgatgga atatagcatt gtagttgact ttttaaaaaa aaaaaaacia      2280
61      aaaaaaaaaa aaggaattcc gagagctgtc actgcctttg aatgctatcc ctgggatagg      2340
62      ggtggcttca gaaccagga agtggccaag gggcacagac tctgctggag gcctgagccg      2400
63      ggggttccat aggagactga caggagacat tttgccttag gccacaaaaa gaagaaggct      2460
64      accccactta cagatgcaga ccattgtggg ctcggagaaa ctgctttagt catggtttct      2520
65      agtgttgga gcagatgga ctactgagca tgtctacaga cccagtcgta gagtgtgtac      2580
66      tgtggggatt tccggagggt ccattctgga gacctttgtg cagcgtgtat accagcctta      2640
67      cctcaccact tgcgacggac acagagcctg cagcacctac cgaaccatct accggactgc      2700
68      ctatcgccgt agccctgggg tgactccgc aaggcctcgc tatgcttgct gccctggttg      2760
69      gaagaggacc agtgggctcc ctggggcttg tggagcagca atatgccagc ctccatgtgg      2820
70      gaatggaggg agttcatccg cccaggacac tgcgctgcc ctgtggatgg caggagagata      2880
71      ttgccagac agatgttgat gaatgcagta caggagaggc cagttgtccc cagcgtgtg      2940
72      tcaatactgt gggaaagtac tgggtgccag gatgggaggg acaaagccca tctgcagatg      3000
73      ggacccctg cctgtctaag gaggggccct cccctttccc cccaaacccc acagcaggag      3060
74      tggacagcat ggcgagagag gaggtgtaca ggtgcaggc tcgggttgat gtgctagaac      3120
75      agaaactgca gttggtgctg gccccactgc acagcctggc ctctcggtcc acagagcatg      3180
76      ggctacaaga tcctggcagc ctgctggtgt ccttcttggg ggaacatctg gggtcctgtg      3240
77      agtccacaaa gacaccactc caccacaga gagcctaggg gacccatggg gtggacacca      3300
78      gggctgggtg gatggaactt cttctgggat gggcagattt gcaagtttac accttttttc      3360
79      ctctcctgcc ctaggctcct gcaaaaaaga tctgtgataa cctctcacca ccaggtgga      3420
80      tagagcagta tccagatccc ttgtagccag agttcaggga cgctgtctgg tgggtcctat      3480
81      gagcagaagc cctgcctcat tgtccctctt tcttaggagg ttcctaggac ttgggtatgg      3540
82      ggagtgggtg cttgtgtgac tcttcagtgg ggctccctgt ctaagtggta aggtggggat      3600
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 506

87 <212> TYPE: PRT

88 <213> ORGANISM: Mus musculus

89 <400> SEQUENCE: 2

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91      1          5          10          15
92      His His Gln Gln Gln Ala Ala Gln Asn Ser Leu Leu Pro Leu Leu Ser
93      20          25          30
94      Ser Ala Val Glu Pro Pro Asp Gln Lys Pro Leu Leu Pro Ile Pro Ile
95      35          40          45
96      Thr Gln Lys Pro Gln Ala Ala Pro Glu Thr Leu Lys Asp Ala Ile Gly
97      50          55          60
98      Ile Lys Lys Glu Lys Pro Lys Thr Ser Phe Val Cys Thr Tyr Cys Ser

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99	65	70	75	80
100	Lys Ala Phe Arg Asp Ser Tyr His Leu Arg Arg His Gln Ser Cys His			
101		85	90	95
102	Thr Gly Ile Lys Leu Val Ser Arg Ala Lys Lys Thr Pro Thr Thr Val			
103		100	105	110
104	Val Pro Leu Ile Ser Thr Ile Ala Gly Asp Ser Ser Arg Thr Ser Leu			
105		115	120	125
106	Val Ser Thr Ile Ala Gly Ile Leu Ser Thr Val Thr Ser Ser Ser			
107		130	135	140
108	Gly Thr Asn Pro Ser Ser Ala Ser Thr Thr Ala Met Pro Val Pro			
109		145	150	155
110	Gln Ser Val Lys Lys Pro Ser Lys Pro Val Lys Lys Asn His Ala Cys			
111		165	170	175
112	Glu Met Cys Gly Lys Ala Phe Arg Asp Val Tyr His Leu Asn Arg His			
113		180	185	190
114	Lys Leu Ser His Ser Asp Glu Lys Pro Phe Glu Cys Pro Ile Cys Asn			
115		195	200	205
116	Gln Arg Phe Lys Arg Lys Asp Arg Met Thr Tyr His Val Arg Ser His			
117		210	215	220
118	Glu Gly Gly Ile Thr Lys Pro Tyr Thr Cys Ser Val Cys Gly Lys Gly			
119		225	230	235
120	Phe Ser Arg Pro Asp His Leu Ser Cys His Val Lys His Val His Ser			
121		245	250	255
122	Thr Glu Arg Pro Phe Lys Cys Gln Thr Cys Thr Ala Ala Phe Ala Thr			
123		260	265	270
124	Lys Asp Arg Leu Arg Thr His Met Val Arg His Glu Gly Lys Val Ser			
125		275	280	285
126	Cys Asn Ile Cys Gly Lys Leu Leu Ser Ala Ala Tyr Ile Thr Ser His			
127		290	295	300
128	Leu Lys Thr His Gly Gln Ser Gln Ser Ile Asn Cys Asn Thr Cys Lys			
129		305	310	315
130	Gln Gly Ile Ser Lys Thr Cys Met Ser Glu Glu Thr Ser Asn Gln Lys			
131		325	330	335
132	Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His			
133		340	345	350
134	Val Thr Ser Trp Pro Gly Lys Gln Val Glu Thr Leu Arg Leu Trp Glu			
135		355	360	365
136	Glu Ala Val Lys Ala Arg Lys Lys Glu Ala Ala Asn Leu Cys Gln Thr			
137		370	375	380
138	Ser Thr Ala Ala Thr Thr Pro Val Thr Leu Thr Thr Pro Phe Asn Ile			
139		385	390	395
140	Thr Ser Ser Val Ser Ser Gly Thr Met Ser Asn Pro Val Thr Val Ala			
141		405	410	415
142	Ala Ala Met Ser Met Arg Ser Pro Val Asn Val Ser Ser Ala Val Asn			
143		420	425	430
144	Ile Thr Ser Pro Leu Ala Met Thr Ser Pro Leu Thr Leu Thr Thr Pro			
145		435	440	445
146	Val Asn Leu Pro Thr Pro Val Thr Ala Pro Val Asn Ile Ala His Pro			
147		450	455	460

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148      Val Thr Ile Thr Ser Pro Met Asn Leu Pro Thr Pro Met Thr Leu Ala
149      465                                470                                475                                480
150      Ala Pro Leu Asn Ile Ala Met Arg Pro Val Glu Ser Met Pro Phe Leu
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152      Pro Gln Ala Leu Pro Thr Ser Pro Pro Trp
153                                500                                505
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156 <211> LENGTH: 2306
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 3
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162      tgctgccctt cctgagctct gccgtggagc cccctgatca gaaaccattg cttccaatac      180
163      caataactca gaaacctcag ggtgcaccag aaacattaaa ggatgccatt gggattaaaa      240
164      aagaaaaacc caaaacttca tttgtgtgca cttactgcag taaagctttc agggacagct      300
165      atcacctgag gcgccacgaa tctgccaca cagggatcaa gttggtgtcc cggccaaaga      360
166      aaacccccac cacggtggtt ccccttatct ctaccatgcg tggggacagc agccgaactt      420
167      cgttggtctc gaccattgca ggcattctgt caacagtac tacatcttcc tcgggcacca      480
168      accccagtag cagtgccagc accacagcta tgccagtgc ccagtctgtc aagaaaccca      540
169      gtaagcctgt caagaagaac catgcttggt agatgtgtgg gaaggccttc cgagatgtgt      600
170      accatctcaa tcgacacaag ctctcccatt cagatgagaa accctttgag tgtcctattt      660
171      gtaatcagcg cttcaagagg aaggaccgga tgacttacca tgtgaggtct catgaaggag      720
172      gcatcaccaa accctatact tgcagtgttt gtgggaaagg cttctcaagg cctgaccact      780
173      taagctgtca tgtaaaacat gtccattcaa cagaaagacc cttcaaatgc caaacgtgca      840
174      ctgctgcctt tgccaccaa gacagatgc ggacacacat ggtgcgccat gaaggcaggg      900
175      tatcatgtaa catctgtggg aagctcctga gtgcagcata catcaccagc cacttaaaga      960
176      ctcatgggca gagccaaagt atcaactgta atacatgtaa acaaggcatc agtaaaacat      1020
177      gcatgagtga agagaccagt aaccaaagc agcagcagca gcagcagcag caacaacaac      1080
178      aacaacaaca tgtgacaagc tggccaggga agcaagtaga aacactcaga ctgtgggaag      1140
179      aagctgttaa agcaaggaag aaagaagctg ctaacctgtg ccaaacctcc acggctgcta      1200
180      cgacacctgt gactctcact actccattca gtataacatc ctctgtgtcg tctgagacta      1260
181      tgtcaaaccc agtcacagtg gcagctgcaa tgagcatgag aagtccagta aatgtttcaa      1320
182      gtgcagttaa cataaccagc ccaatgaaca tagggcatcc tgtaactata accagtccat      1380
183      tatccatgac ctctccttta aactcacta cccagtcaa cctccccacc cccgtcactg      1440
184      cccagtgaa tatagcacac cctgtcacca tcacatctcc aatgaatcta cccacaccta      1500
185      tgacattagc cgccctctc aatatagcaa tgagacctgt agagagcatg cctttcttgc      1560
186      cccaagcttt gectacatca ccgccttggg aaacagtatt ataaaatcaa aatatgggta      1620
187      aaagtaaata tttaccagca acttaacttt tagttgatta aagcaaaaag taaaccatga      1680
188      aattgggaga ttttattaca ttagttaata agagtgtggt agcatttttc tccaatttgg      1740
189      ctgggattat tcaaagtagg gtgtgtatgt aacttatcac tggaccactt tagtttaatc      1800
190      agaaattcct tttagctgac aacattgctt aaacaggata gtagttggca agatgaaatg      1860
191      ccagaattaa aaccaatcat aagtagaacc cacttcaaaa taaaaaaaca gcattactat      1920
192      ttctaattccc aaggaatcac tttattgtaa acactagcag aactcttctc cctatacaag      1980
193      gtggatggct gattttaacc tgaaatttta aatccacaga ttgagagcta gtgtagaatt      2040
194      gtctgtgttt attgttttta tgagtaaata catgcattgt cataataaaa tgcatttcag      2100
195      agaatatgca ttttaccttt gggaaatatg taatttcagg cagcattccc tatgggaaag      2160
196      gtgataccag ctctgatatg caaagcatat gataatttat cattctaact tcaacgtata      2220
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201 <211> LENGTH: 516
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 4
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207      His His Gln Gln Ala Ala Gln Asn Ser Leu Leu Pro Leu Leu Ser
208           20             25             30
209      Ser Ala Val Glu Pro Pro Asp Gln Lys Pro Leu Leu Pro Ile Pro Ile
210           35             40             45
211      Thr Gln Lys Pro Gln Gly Ala Pro Glu Thr Leu Lys Asp Ala Ile Gly
212           50             55             60
213      Ile Lys Lys Glu Lys Pro Lys Thr Ser Phe Val Cys Thr Tyr Cys Ser
214           65             70             75             80
215      Lys Ala Phe Arg Asp Ser Tyr His Leu Arg Arg His Glu Ser Cys His
216           85             90             95
217      Thr Gly Ile Lys Leu Val Ser Arg Pro Lys Lys Thr Pro Thr Thr Val
218           100            105            110
219      Val Pro Leu Ile Ser Thr Ile Ala Gly Asp Ser Ser Arg Thr Ser Leu
220           115            120            125
221      Val Ser Thr Ile Ala Gly Ile Leu Ser Thr Val Thr Ser Ser Ser
222           130            135            140
223      Gly Thr Asn Pro Ser Ser Ser Ala Ser Thr Thr Ala Met Pro Val Thr
224           145            150            155            160
225      Gln Ser Val Lys Lys Pro Ser Lys Pro Val Lys Lys Asn His Ala Cys
226           165            170            175
227      Glu Met Cys Gly Lys Ala Phe Arg Asp Val Tyr His Leu Asn Arg His
228           180            185            190
229      Lys Leu Ser His Ser Asp Glu Lys Pro Phe Glu Cys Pro Ile Cys Asn
230           195            200            205
231      Gln Arg Phe Lys Arg Lys Asp Arg Met Thr Tyr His Val Arg Ser His
232           210            215            220
233      Glu Gly Gly Ile Thr Lys Pro Tyr Thr Cys Ser Val Cys Gly Lys Gly
234           225            230            235            240
235      Phe Ser Arg Pro Asp His Leu Ser Cys His Val Lys His Val His Ser
236           245            250            255
237      Thr Glu Arg Pro Phe Lys Cys Gln Thr Cys Thr Ala Ala Phe Ala Thr
238           260            265            270
239      Lys Asp Arg Leu Arg Thr His Met Val Arg His Glu Gly Lys Val Ser
240           275            280            285
241      Cys Asn Ile Cys Gly Lys Leu Leu Ser Ala Ala Tyr Ile Thr Ser His
242           290            295            300
243      Leu Lys Thr His Gly Gln Ser Gln Ser Ile Asn Cys Asn Thr Cys Lys
244           305            310            315            320
245      Gln Gly Ile Ser Lys Thr Cys Met Ser Glu Glu Thr Ser Asn Gln Lys
246           325            330            335
247      Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Val Thr

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